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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/047,412A

DATE: 04/26/2002

TIME: 11:45:53

Input Set : A:\30780DIV1 revised sequence listing v2.txt

Output Set: N:\CRF3\04262002\J047412A.raw

3 <110> APPLICANT: Levin, Joshua Z.
4 Budziszewski, Gregory J.
5 Potter, Sharon L.
6 Wegrich, Lynette M.
8 <120> TITLE OF INVENTION: Herbicide Target Genes and Methods
10 <130> FILE REFERENCE: PB/5-30780DIV
12 <140> CURRENT APPLICATION NUMBER: 10/047,412A
C--> 13 <141> CURRENT FILING DATE: 2002-04-11
15 <160> NUMBER OF SEQ ID NOS: 29
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1119
21 <212> TYPE: DNA
22 <213> ORGANISM: Arabidopsis thaliana
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(1119)
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31 1 5 10 15
33 aag aag aag att aaa gat gtt gtt ctt aag gct gag atg ttt gca ccg 96
34 Lys Lys Lys Ile Lys Asp Val Val Leu Lys Ala Glu Met Phe Ala Pro
35 20 25 30
37 gat gct ctt gag ctt gaa gaa gag cag tgg ata aag caa gaa gaa aca 144
38 Asp Ala Leu Glu Leu Glu Glu Glu Gln Trp Ile Lys Gln Glu Glu Thr
39 35 40 45
41 atg cgt tac ttt gat tta tgg gat gat ccc gct aaa tct gat gag att 192
42 Met Arg Tyr Phe Asp Leu Trp Asp Asp Pro Ala Lys Ser Asp Glu Ile
43 50 55 60
45 ctt ctc aaa tta gct gat cga gct aaa gca gtc gat tcc ctc aaa gac 240
46 Leu Leu Lys Leu Ala Asp Arg Ala Lys Ala Val Asp Ser Leu Lys Asp
47 65 70 75 80
49 ctc aaa tac aag gct gaa gaa gct aag ctg atc ata caa ttg ggt gag 288
50 Leu Lys Tyr Lys Ala Glu Glu Ala Lys Leu Ile Ile Gln Leu Gly Glu
51 85 90 95
53 atg gat gct ata gat tac agt ctc ttt gag caa gcc tat gat tca tca 336
54 Met Asp Ala Ile Asp Tyr Ser Leu Phe Glu Gln Ala Tyr Asp Ser Ser
55 100 105 110
57 ctc gat gta agt aga tcg ttg cat cac tat gag atg tct aag ctt ctt 384
58 Leu Asp Val Ser Arg Ser Leu His His Tyr Glu Met Ser Lys Leu Leu
59 115 120 125
61 agg gat caa tat gac gct gaa ggc gct tgt atg att atc aaa tct gga 432

ENTERED

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62 Arg Asp Gln Tyr Asp Ala Glu Gly Ala Cys Met Ile Ile Lys Ser Gly
63      130      135      140
65 tct cca ggc gca aaa tct cag ata tgg aca gag caa gtt gta agt atg 480
66 Ser Pro Gly Ala Lys Ser Gln Ile Trp Thr Glu Gln Val Val Ser Met
67 145      150      155      160
69 tat atc aaa tgg gca gaa agg cta ggc caa aac gcg cgg gtg gct gag 528
70 Tyr Ile Lys Trp Ala Glu Arg Leu Gly Gln Asn Ala Arg Val Ala Glu
71      165      170      175
73 aaa tgt agt tta ttg agt aat aaa agt ggc gta agt tca gcc acg ata 576
74 Lys Cys Ser Leu Leu Ser Asn Lys Ser Gly Val Ser Ser Ala Thr Ile
75      180      185      190
77 gag ttt gaa ttc gag ttt gct tat ggt tat ctc tta ggt gag cga ggt 624
78 Glu Phe Glu Phe Glu Phe Ala Tyr Gly Tyr Leu Leu Gly Glu Arg Gly
79      195      200      205
81 gtg cac cgc ctt atc ata agt tcc act tct aat gag gaa tgt tca gcg 672
82 Val His Arg Leu Ile Ile Ser Ser Thr Ser Asn Glu Glu Cys Ser Ala
83      210      215      220
85 act gtt gat atc ata cca cta ttc ttg aga gca tct cct gat ttt gaa 720
86 Thr Val Asp Ile Ile Pro Leu Phe Leu Arg Ala Ser Pro Asp Phe Glu
87 225      230      235      240
89 gta aag gaa ggt gat ttg att gta tcg tat cct gca aaa gag gat cac 768
90 Val Lys Glu Gly Asp Leu Ile Val Ser Tyr Pro Ala Lys Glu Asp His
91      245      250      255
93 aaa ata gct gag aat atg gtt tgt atc cac cat att ccg agt gga gta 816
94 Lys Ile Ala Glu Asn Met Val Cys Ile His His Ile Pro Ser Gly Val
95      260      265      270
97 aca cta caa tct tca gga gaa aga aac cgg ttt gca aac agg atc aaa 864
98 Thr Leu Gln Ser Ser Gly Glu Arg Asn Arg Phe Ala Asn Arg Ile Lys
99      275      280      285
101 gct cta aac cgg ttg aag gcg aag cta ctt gtg ata gca aaa gag caa 912
102 Ala Leu Asn Arg Leu Lys Ala Lys Leu Leu Val Ile Ala Lys Glu Gln
103      290      295      300
105 aag gtt tcg gat gta aat aaa atc gac agc aag aac att ttg gaa ccg 960
106 Lys Val Ser Asp Val Asn Lys Ile Asp Ser Lys Asn Ile Leu Glu Pro
107 305      310      315      320
109 cgg gaa gaa acc agg agt tat gtc tct aag ggt cac aag atg gtg gtt 1008
110 Arg Glu Glu Thr Arg Ser Tyr Val Ser Lys Gly His Lys Met Val Val
111      325      330      335
113 gat aga aaa acc ggt tta gag att ctg gac ctg aaa tcg gtc ttg gat 1056
114 Asp Arg Lys Thr Gly Leu Glu Ile Leu Asp Leu Lys Ser Val Leu Asp
115      340      345      350
117 gga aac att gga cca ctc ctt gga gct cat att agc atg aga aga tca 1104
118 Gly Asn Ile Gly Pro Leu Leu Gly Ala His Ile Ser Met Arg Arg Ser
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121 att gat gcg att tag 1119
122 Ile Asp Ala Ile
123      370
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 372
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128 <212> TYPE: PRT
129 <213> ORGANISM: Arabidopsis thaliana
131 <400> SEQUENCE: 2
132 Met Asp Asp Met Asp Thr Val Tyr Lys Gln Leu Gly Leu Phe Ser Leu
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134 Lys Lys Lys Ile Lys Asp Val Val Leu Lys Ala Glu Met Phe Ala Pro
135 20 25 30
136 Asp Ala Leu Glu Leu Glu Glu Glu Gln Trp Ile Lys Gln Glu Glu Thr
137 35 40 45
138 Met Arg Tyr Phe Asp Leu Trp Asp Asp Pro Ala Lys Ser Asp Glu Ile
139 50 55 60
140 Leu Leu Lys Leu Ala Asp Arg Ala Lys Ala Val Asp Ser Leu Lys Asp
141 65 70 75 80
142 Leu Lys Tyr Lys Ala Glu Glu Ala Lys Leu Ile Ile Gln Leu Gly Glu
143 85 90 95
144 Met Asp Ala Ile Asp Tyr Ser Leu Phe Glu Gln Ala Tyr Asp Ser Ser
145 100 105 110
146 Leu Asp Val Ser Arg Ser Leu His His Tyr Glu Met Ser Lys Leu Leu
147 115 120 125
148 Arg Asp Gln Tyr Asp Ala Glu Gly Ala Cys Met Ile Ile Lys Ser Gly
149 130 135 140
150 Ser Pro Gly Ala Lys Ser Gln Ile Trp Thr Glu Gln Val Val Ser Met
151 145 150 155 160
152 Tyr Ile Lys Trp Ala Glu Arg Leu Gly Gln Asn Ala Arg Val Ala Glu
153 165 170 175
154 Lys Cys Ser Leu Leu Ser Asn Lys Ser Gly Val Ser Ser Ala Thr Ile
155 180 185 190
156 Glu Phe Glu Phe Glu Phe Ala Tyr Gly Tyr Leu Leu Gly Glu Arg Gly
157 195 200 205
158 Val His Arg Leu Ile Ile Ser Ser Thr Ser Asn Glu Glu Cys Ser Ala
159 210 215 220
160 Thr Val Asp Ile Ile Pro Leu Phe Leu Arg Ala Ser Pro Asp Phe Glu
161 225 230 235 240
162 Val Lys Glu Gly Asp Leu Ile Val Ser Tyr Pro Ala Lys Glu Asp His
163 245 250 255
164 Lys Ile Ala Glu Asn Met Val Cys Ile His His Ile Pro Ser Gly Val
165 260 265 270
166 Thr Leu Gln Ser Ser Gly Glu Arg Asn Arg Phe Ala Asn Arg Ile Lys
167 275 280 285
168 Ala Leu Asn Arg Leu Lys Ala Lys Leu Leu Val Ile Ala Lys Glu Gln
169 290 295 300
170 Lys Val Ser Asp Val Asn Lys Ile Asp Ser Lys Asn Ile Leu Glu Pro
171 305 310 315 320
172 Arg Glu Glu Thr Arg Ser Tyr Val Ser Lys Gly His Lys Met Val Val
173 325 330 335
174 Asp Arg Lys Thr Gly Leu Glu Ile Leu Asp Leu Lys Ser Val Leu Asp
175 340 345 350
176 Gly Asn Ile Gly Pro Leu Leu Gly Ala His Ile Ser Met Arg Arg Ser
177 355 360 365

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179 370
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184 <211> LENGTH: 1458
185 <212> TYPE: DNA
186 <213> ORGANISM: Arabidopsis thaliana
188 <220> FEATURE:
189 <221> NAME/KEY: CDS
190 <222> LOCATION: (1)..(1458)
192 <400> SEQUENCE: 3
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195 1 5 10 15
197 gac aat gaa gca gaa ttg gac gag aat gat ggt gat gtt gga aag gaa 96
198 Asp Asn Glu Ala Glu Leu Asp Glu Asn Asp Gly Asp Val Gly Lys Glu
199 20 25 30
201 gaa gaa gat gtt gat atg gat atg gct gat tta gag aca ctt aac tat 144
202 Glu Glu Asp Val Asp Met Asp Met Ala Asp Leu Glu Thr Leu Asn Tyr
203 35 40 45
205 gat gat ctc gat aat gtt tct aag ctg cag aag agt cag aga tat gct 192
206 Asp Asp Leu Asp Asn Val Ser Lys Leu Gln Lys Ser Gln Arg Tyr Ala
207 50 55 60
209 gat att atg cat aaa gta gag gag gct ctt ggg aaa gat tct gat gga 240
210 Asp Ile Met His Lys Val Glu Glu Ala Leu Gly Lys Asp Ser Asp Gly
211 65 70 75 80
213 gct gag aaa gga act gtc ttg gaa gat gat cct gag tat aag ctt att 288
214 Ala Glu Lys Gly Thr Val Leu Glu Asp Asp Pro Glu Tyr Lys Leu Ile
215 85 90 95
217 gtg gat tgt aat cag ctt tcg gtc gat att gag aat gaa atc gtt att 336
218 Val Asp Cys Asn Gln Leu Ser Val Asp Ile Glu Asn Glu Ile Val Ile
219 100 105 110
221 gtc cac aac ttt atc aaa gac aag tac aag ctt aag ttt caa gag ctt 384
222 Val His Asn Phe Ile Lys Asp Lys Tyr Lys Leu Lys Phe Gln Glu Leu
223 115 120 125
225 gag tcg ttg gtt cat cac cct att gac tat gca tgt gtt gtg aag aag 432
226 Glu Ser Leu Val His His Pro Ile Asp Tyr Ala Cys Val Val Lys Lys
227 130 135 140
229 att ggg aat gag acg gat ttg gct ctt gtt gat ctc gct gac ctt ctt 480
230 Ile Gly Asn Glu Thr Asp Leu Ala Leu Val Asp Leu Ala Asp Leu Leu
231 145 150 155 160
233 cct tca gct att atc atg gtt gtt tca gtt act gct tta act acg aaa 528
234 Pro Ser Ala Ile Ile Met Val Val Ser Val Thr Ala Leu Thr Thr Lys
235 165 170 175
237 ggg agt gca ctg cca gag gat gtt ttg caa aag gtg tta gag gct tgt 576
238 Gly Ser Ala Leu Pro Glu Asp Val Leu Gln Lys Val Leu Glu Ala Cys
239 180 185 190
241 gat cgg gct tta gat ctt gat tcc gca agg aag aag gtc ctt gag ttt 624
242 Asp Arg Ala Leu Asp Leu Asp Ser Ala Arg Lys Lys Val Leu Glu Phe
243 195 200 205

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245	gtt	gaa	agt	aag	atg	gga	tct	att	gca	cct	aat	ctt	tct	gct	att	gtt	672
246	Val	Glu	Ser	Lys	Met	Gly	Ser	Ile	Ala	Pro	Asn	Leu	Ser	Ala	Ile	Val	
247		210					215					220					
249	ggg	agt	gct	gtt	gca	gcc	aaa	ctc	atg	ggg	act	gct	gga	ggt	ttg	tca	720
250	Gly	Ser	Ala	Val	Ala	Ala	Lys	Leu	Met	Gly	Thr	Ala	Gly	Gly	Leu	Ser	
251	225					230					235					240	
253	gca	ctt	gct	aaa	atg	cct	gcg	tgt	aat	gtt	caa	gtt	ctt	ggc	cac	aag	768
254	Ala	Leu	Ala	Lys	Met	Pro	Ala	Cys	Asn	Val	Gln	Val	Leu	Gly	His	Lys	
255				245						250					255		
257	agg	aag	aac	ctt	gct	ggg	ttt	tct	tct	gca	acg	tct	cag	tcc	cgt	gtg	816
258	Arg	Lys	Asn	Leu	Ala	Gly	Phe	Ser	Ser	Ala	Thr	Ser	Gln	Ser	Arg	Val	
259			260						265					270			
261	ggt	tat	ctg	gag	cag	aca	gag	att	tac	caa	agc	acg	cct	cct	gga	ctt	864
262	Gly	Tyr	Leu	Glu	Gln	Thr	Glu	Ile	Tyr	Gln	Ser	Thr	Pro	Pro	Gly	Leu	
263			275					280					285				
265	cag	gct	cgc	gct	ggc	agg	ctc	gtg	gct	gca	aaa	tca	act	ttg	gca	gca	912
266	Gln	Ala	Arg	Ala	Gly	Arg	Leu	Val	Ala	Ala	Lys	Ser	Thr	Leu	Ala	Ala	
267		290					295					300					
269	aga	gtt	gat	gct	act	aga	ggg	gat	ccg	tta	ggg	ata	agt	gga	aaa	gct	960
270	Arg	Val	Asp	Ala	Thr	Arg	Gly	Asp	Pro	Leu	Gly	Ile	Ser	Gly	Lys	Ala	
271	305					310					315					320	
273	ttc	agg	gag	gag	atc	cgt	aag	aag	att	gag	aaa	tgg	caa	gaa	cct	cct	1008
274	Phe	Arg	Glu	Glu	Ile	Arg	Lys	Lys	Ile	Glu	Lys	Trp	Gln	Glu	Pro	Pro	
275				325					330						335		
277	cct	gca	aga	cag	cct	aag	cca	ctt	cct	gtt	cct	gat	tct	gaa	ccg	aag	1056
278	Pro	Ala	Arg	Gln	Pro	Lys	Pro	Leu	Pro	Val	Pro	Asp	Ser	Glu	Pro	Lys	
279			340					345						350			
281	aaa	aga	agg	ggt	ggt	cgc	cgt	cta	aga	aaa	atg	aaa	gaa	agg	tat	caa	1104
282	Lys	Arg	Arg	Gly	Gly	Arg	Arg	Leu	Arg	Lys	Met	Lys	Glu	Arg	Tyr	Gln	
283			355					360					365				
285	gta	aca	gat	atg	agg	aag	ctg	gcc	aac	aga	atg	gcg	ttt	ggt	aca	cct	1152
286	Val	Thr	Asp	Met	Arg	Lys	Leu	Ala	Asn	Arg	Met	Ala	Phe	Gly	Thr	Pro	
287		370					375					380					
289	gaa	gag	agc	tcc	ctc	ggt	gat	gga	cta	gga	gaa	ggt	tat	gga	atg	ctt	1200
290	Glu	Glu	Ser	Ser	Leu	Gly	Asp	Gly	Leu	Gly	Glu	Gly	Tyr	Gly	Met	Leu	
291	385					390					395					400	
293	ggc	cag	gca	gga	agc	aac	agg	ctg	cga	gta	tcc	agt	gtt	ccg	agc	aag	1248
294	Gly	Gln	Ala	Gly	Ser	Asn	Arg	Leu	Arg	Val	Ser	Ser	Val	Pro	Ser	Lys	
295				405						410					415		
297	ctt	aag	att	aat	gct	aag	gtc	gcc	aaa	aag	ctt	aaa	gaa	agg	cag	tat	1296
298	Leu	Lys	Ile	Asn	Ala	Lys	Val	Ala	Lys	Lys	Leu	Lys	Glu	Arg	Gln	Tyr	
299			420						425						430		
301	gcg	ggt	ggt	gcg	act	acc	tct	ggt	ttg	aca	tcg	agc	ctg	gct	ttc	act	1344
302	Ala	Gly	Gly	Ala	Thr	Thr	Ser	Gly	Leu	Thr	Ser	Ser	Leu	Ala	Phe	Thr	
303			435					440					445				
305	cct	gtg	cag	gga	ata	gag	ttg	tgc	aat	cct	cag	cag	gct	tta	gga	tta	1392
306	Pro	Val	Gln	Gly	Ile	Glu	Leu	Cys	Asn	Pro	Gln	Gln	Ala	Leu	Gly	Leu	
307		450					455					460					
309	gga	agt	ggg	act	caa	agc	act	tac	ttc	tca	gag	tca	gga	acc	ttc	tcg	1440

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 19

Seq#:29; Xaa Pos. 39,155,162,187,465